

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/595,562
Source: IFWP
Date Processed by STIC: 2/1/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/595,562

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text.**

5 Variable Length Sequence(s) 1, 2, 3, 56, 61, 69 contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213> Response Per 1.823 of Sequence Rules, the **only valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/595,562

DATE: 02/01/2007
TIME: 12:08:51

Input Set : A:\PTO.SS.TXT
Output Set: N:\CRF4\02012007\J595562.raw

52 <223> OTHER INFORMATION: Xaa can be any residue

54 <400> SEQUENCE: 1 / / / /

W--> 56 Asn Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Pro
E--> 57 1 5 10

60 <210> SEQ ID NO: 2 21179 insert this mandatory residue identifier
61 <212> TYPE: PRT

62 <213> ORGANISM: Homo sapiens
65 <220> FEATURE:
66 <221> NAME/KEY: misc_feature
67 <222> LOCATION: (2)..(2)
68 <223> OTHER INFORMATION: Xaa (1-16 repeats) can be any residue
70 <220> FEATURE:
71 <221> NAME/KEY: misc_feature
72 <222> LOCATION: (3)..(3)
73 <223> OTHER INFORMATION: Xaa can be Arg, Lys, His or Gln
75 <220> FEATURE:
76 <221> NAME/KEY: misc_feature
77 <222> LOCATION: (4)..(4)
78 <223> OTHER INFORMATION: Xaa (2-3 repeats) can be any residue or a hydrophobic residue
or an equivalent thereof
79 <220> FEATURE:
80 <221> NAME/KEY: misc_feature
83 <222> LOCATION: (5)..(5)
84 <223> OTHER INFORMATION: Xaa is serine or threonine
86 <220> FEATURE:
87 <221> NAME/KEY: misc_feature
88 <222> LOCATION: (6)..(6)
89 <223> OTHER INFORMATION: Xaa can be any residue

92 <400> SEQUENCE: 2 / / / /

W--> 94 Tyr Xaa Xaa Xaa Xaa Xaa Pro
E--> 95 1 5

98 <210> SEQ ID NO: 3 21179

99 <212> TYPE: PRT

100 <213> ORGANISM: Homo sapiens
103 <220> FEATURE:
104 <221> NAME/KEY: misc_feature
105 <222> LOCATION: (2)..(3)
106 <223> OTHER INFORMATION: Xaa can be any residue
108 <220> FEATURE:
109 <221> NAME/KEY: misc_feature
110 <222> LOCATION: (4)..(4)
111 <223> OTHER INFORMATION: Tyr is phosphotyrosine
113 <220> FEATURE:
114 <221> NAME/KEY: misc_feature
115 <222> LOCATION: (5)..(5)
116 <223> OTHER INFORMATION: Xaa (1-30 repeats) can be any residue
118 <220> FEATURE:

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119 <221> NAME/KEY: misc_feature
120 <222> LOCATION: (6)..(6)
121 <223> OTHER INFORMATION: Xaa can be Arg, Lys, His or Gln
123 <220> FEATURE:
124 <221> NAME/KEY: misc_feature
125 <222> LOCATION: (7)..(7)
126 <223> OTHER INFORMATION: Xaa (1-4 repeats) can be any residue
128 <220> FEATURE:
129 <221> NAME/KEY: misc_feature
130 <222> LOCATION: (8)..(8)
131 <223> OTHER INFORMATION: Xaa is phosphoserine or phosphothreonine
133 <220> FEATURE:
134 <221> NAME/KEY: misc_feature
135 <222> LOCATION: (9)..(9)
136 <223> OTHER INFORMATION: Xaa can be any residue

138 <400> SEQUENCE: 3 / / / / /
W--> 140 Asn Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa
E--> 141 1 5
144 <210> SEQ ID NO: 4 → 211714
145 <212> TYPE: PRT
146 <213> ORGANISM: Homo sapiens

148 <400> SEQUENCE: 4
E--> 150 Asn Gly Pro Tyr Leu Gly Pro Pro... His Ser Arg Ser Leu Pro
E--> 151 1 5
154 <210> SEQ ID NO: 5 → 211713
155 <212> TYPE: PRT
156 <213> ORGANISM: Homo sapiens

158 <400> SEQUENCE: 5
E--> 160 Asn Val His Tyr Arg Thr Pro... Lys Thr His Thr Met Pro
E--> 161 1 5
164 <210> SEQ ID NO: 6 → 211715
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapiens

168 <400> SEQUENCE: 6
E--> 170 Arg Tyr Phe Thr Gln Lys Glu Glu Thr Glu Ser Gly Ser Gly Pro
E--> 171 1 5
174 <210> SEQ ID NO: 7 → 211722
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens

178 <400> SEQUENCE: 7
E--> 180 Asn Lys Lys Tyr Glu Leu Gln Asp Arg Asp Val Cys Glu Pro... Arg Tyr
181 1 5 10
E--> 184 Arg Ser Val Ser Glu Pro
188 <210> SEQ ID NO: 8 → 20

These are invalid. If you are denoting a gap, delete the 2 Pro's, and begin a new SEQ ID NO with this group.

Otherwise, number the amino acids.

same error

same error

same error

same error

delete
**

Arg Tyr Phe Thr Gln Lys Glu Glu Thr Glu Ser Gly Ser Gly Pro

171 1 5 10 15

Arg Ser Val Ser Glu Pro

188 <210> SEQ ID NO: 8 → 20

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Input Set : A:\PTO.SS.TXT
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(211713

189 <212> TYPE: PRT
190 <213> ORGANISM: Homo sapiens

192 <400> SEQUENCE: 8
E--> 194 Asn Pro Thr Tyr Ser Val Met Arg Ser His Ser Tyr Pro
E--> 195 1 5 10

198 <210> SEQ ID NO: 9 (211724
199 <212> TYPE: PRT

200 <213> ORGANISM: Homo sapiens

202 <400> SEQUENCE: 9
E--> 204 Asn Ile Phe Tyr Leu Ile Arg Lys Ser Gly Ser Phe Pro Met Pro Glu
E--> 205 1 5 10 15
E--> 208 Leu Lys Leu Ser Ile Ser Phe Pro
212 <210> SEQ ID NO: 10 (211719
213 <212> TYPE: PRT
214 <213> ORGANISM: Homo sapiens

216 <400> SEQUENCE: 10
E--> 218 Asn Glu Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro
E--> 219 1 5 10 15
E--> 222 Ser Tyr Pro
226 <210> SEQ ID NO: 11 (211719
227 <212> TYPE: PRT
228 <213> ORGANISM: Homo sapiens

230 <400> SEQUENCE: 11
E--> 232 Asn Gln Glu Tyr Leu Asp Leu Ser Met Pro Leu Asp Gln Tyr Ser Pro
E--> 233 1 5 10 15
E--> 236 Ser Phe Pro
240 <210> SEQ ID NO: 12 (211716
241 <212> TYPE: PRT
242 <213> ORGANISM: Homo sapiens

244 <400> SEQUENCE: 12
E--> 246 Asn Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro
E--> 247 1 5 10 15
250 <210> SEQ ID NO: 13 (211711
251 <212> TYPE: PRT
252 <213> ORGANISM: Homo sapiens

254 <400> SEQUENCE: 13
E--> 256 Asn Pro Glu Tyr His Ser Ala Ser Ser Gly Pro
E--> 257 1 5 10
260 <210> SEQ ID NO: 14 (211710
261 <212> TYPE: PRT
262 <213> ORGANISM: Homo sapiens

264 <400> SEQUENCE: 14

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E--> 266 Asn Pro Asp Tyr.....Trp Asn His Ser Leu Pro

E--> 267 1 S 10

270 <210> SEQ ID NO: 15

271 <212> TYPE: PRT

272 <213> ORGANISM: Homo sapiens

274 <400> SEQUENCE: 15

E--> 276 Asn Pro Ser Tyr Ser Ser Asn Pro Phe Val Asn Tyr Asn.....Lys Thr Ser

E--> 277 1 5 10

E--> 280 Ile Cys Ser Lys Ser Asn Pro

284 <210> SEQ ID NO: 16

285 <212> TYPE: PRT

286 <213> ORGANISM: Homo sapiens

288 <400> SEQUENCE: 16

E--> 290 Asn Thr Leu Tyr.....Phe Asn Ser Gln Ser Ser Pro

E--> 291 1 S 10

294 <210> SEQ ID NO: 17

295 <212> TYPE: PRT

296 <213> ORGANISM: Homo sapiens

298 <400> SEQUENCE: 17

E--> 300 Asn Pro Val Tyr Gln Lys Thr Thr Glu Asp Glu Val His Ile.....Cys His

E--> 301 1 5 10

E--> 304 Asn Gln Asp Gly Tyr Ser Tyr Pro

308 <210> SEQ ID NO: 18

309 <212> TYPE: PRT

310 <213> ORGANISM: Homo sapiens

312 <400> SEQUENCE: 18

314 Asn Pro Val Tyr Leu Lys Thr Thr Glu Glu Asp Leu Ser Ile Asp Ile

315 1 5 10 15

E--> 318 Gly...Arg His...Ser Ala Ser Val Gly

341 <210> SEQ ID NO: 20

342 <212> TYPE: PRT

343 <213> ORGANISM: Homo sapiens

E--> 345 <211> LENGTH:

345 <400> SEQUENCE: 20

E--> 347 Asn Pro Ile Tyr.....Lys Ser Ala Val Thr Thr Val Val

E--> 348 1

351 <210> SEQ ID NO: 21

352 <212> TYPE: PRT

353 <213> ORGANISM: Homo sapiens

E--> 355 <211> LENGTH:

355 <400> SEQUENCE: 21

E--> 357 Asn Pro Leu Tyr.....Lys Ser Ala Ile Thr Thr Val Val

E--> 358 1

361 <210> SEQ ID NO: 22

362 <212> TYPE: PRT

same error
as above

RAW SEQUENCE LISTING
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Input Set : A:\PTO.SS.TXT
Output Set: N:\CRF4\02012007\J595562.raw

363 <213> ORGANISM: Homo sapiens
 E--> 365 <211> LENGTH:
 365 <400> SEQUENCE: 22
 E--> 367 Asn Pro Leu Tyr.....Lys Glu Ala Thr Ser Thr Phe Thr
 E--> 368 1
 371 <210> SEQ ID NO: 23
 372 <212> TYPE: PRT
 373 <213> ORGANISM: Homo sapiens
 E--> 375 <211> LENGTH:
 375 <400> SEQUENCE: 23
 E--> 377 Asn Pro Leu Tyr.....Arg Lys Pro Ile Ser Thr His Thr
 E--> 378 1
 381 <210> SEQ ID NO: 24
 382 <212> TYPE: PRT
 383 <213> ORGANISM: Homo sapiens
 E--> 385 <211> LENGTH:
 385 <400> SEQUENCE: 24
 E--> 387 Asn Pro Leu Tyr.....Arg Gly Ser Thr Ser Thr Phe Lys
 E--> 388 1
 391 <210> SEQ ID NO: 25
 392 <212> TYPE: PRT
 393 <213> ORGANISM: Homo sapiens
 E--> 395 <211> LENGTH:
 395 <400> SEQUENCE: 25
 E--> 397 Pro Gly His Tyr Leu.....Arg Cys Asp Ser Thr Gln Pro
 E--> 398 1 5
 421 <210> SEQ ID NO: 28
 422 <212> TYPE: PRT
 423 <213> ORGANISM: Homo sapiens
 E--> 425 <211> LENGTH:
 425 <400> SEQUENCE: 28
 E--> 427 His Ser Gly Tyr Arg His Gln Val Pro Ser Val Gln Val Phe.....Ser Arg
 E--> 428 1 5 10
 E--> 431 Ser Glu Ser Thr Gln Pro
 435 <210> SEQ ID NO: 29
 436 <212> TYPE: PRT
 437 <213> ORGANISM: Homo sapiens
 E--> 439 <211> LENGTH:
 439 <400> SEQUENCE: 29
 E--> 441 Trp Lys Met Tyr Glu Val Tyr Asp Ala.....Lys Ser Lys Ser Val Ser Leu
 E--> 442 1 5
 E--> 445 Pro
 502 <210> SEQ ID NO: 34
 503 <212> TYPE: PRT
 504 <213> ORGANISM: Homo sapiens
 E--> 506 <211> LENGTH:
 506 <400> SEQUENCE: 34
 E--> 508 Glu Glu Ile Tyr Ile Ile Met.....Gln Ser Cys Trp Ala Phe Asp Ser
 E--> 509 Arg

global
errors

same errors
in segs. 26, 27

same errors in segs. 30-32

same errors in segs. 35-39

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Input Set : A:\PTO.SS.TXT
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E--> 510 1 5
E--> 513 Lys Arg Pro Ser Phe Pro
547 <210> SEQ ID NO: 38
548 <212> TYPE: PRT
549 <213> ORGANISM: Homo sapiens
E--> 551 <211> LENGTH:
551 <400> SEQUENCE: 38
E--> 553 Leu Val Ala Tyr Ile Ala Phe Lys Arg Trp Asn Ser Cys Lys Gln Asn.....
554 1 5 10 15
E--> 557Lys Gln Gly Ala Asn Ser Arg Pro Val Asn Gln Thr Pro Pro Pro Glu
E--> 561 Gly Glu Lys Leu His Ser Asp Ser Gly Ile Ser
584 <210> SEQ ID NO: 41
585 <212> TYPE: PRT
586 <213> ORGANISM: Homo sapiens
E--> 588 <211> LENGTH:
588 <400> SEQUENCE: 41
590 Asn Pro Asn Tyr Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro
E--> 591 1 5 10 15 20 25
E--> 594 Trp Thr.....Lys Val Phe Lys Ser Arg Thr Pro Pro
650 <210> SEQ ID NO: 46 20 25
651 <212> TYPE: PRT
652 <213> ORGANISM: Homo sapiens
E--> 654 <211> LENGTH:
654 <400> SEQUENCE: 46 same error in Seq 42-45
E--> 656 Asn Gln Glu Tyr.....Leu Asp Leu Ser Ile Pro Leu Asp Gln Tyr Ser Pro
E--> 657 1
E--> 660 Ser Phe Pro
664 <210> SEQ ID NO: 47
665 <212> TYPE: PRT
666 <213> ORGANISM: Homo sapiens
E--> 668 <211> LENGTH:
668 <400> SEQUENCE: 47
E--> 670 Asn Glu Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu.....Gln Tyr Ser Pro
E--> 671 1 5 10
E--> 674 Ser Tyr
678 <210> SEQ ID NO: 48
679 <212> TYPE: PRT
680 <213> ORGANISM: Homo sapiens
E--> 682 <211> LENGTH:
682 <400> SEQUENCE: 48
E--> 684 Asn Ala Thr Tyr Lys Val Asp Val Ile.....Gln Arg Thr Arg Ser Lys
E--> 685 Pro
E--> 686 1 5 10
689 <210> SEQ ID NO: 49
690 <212> TYPE: PRT
691 <213> ORGANISM: Homo sapiens
E--> 693 <211> LENGTH:
693 <400> SEQUENCE: 49
695 Asn Pro Thr Tyr Lys Met Tyr Glu Gly Gly Glu Pro Asp Asp Val Gly

same

error in Seq
39-40

← misaligned
nos. (see
item 3
in Error
summary
sheet)

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same

696 1 5 10 15
E--> 699 Gly Leu Leu Asp Ala Asp Phe Ala Leu Asp Pro Asp.....Lys Pro Thr Asn
E--> 700 20 25
E--> 703 Phe Thr Asn Pro

same errors in Segs. 50-55, 57-59.

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Input Set : A:\PTO.SS.TXT
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:31; Line(s) 465
Seq#:34; Line(s) 508
Seq#:48; Line(s) 684

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Input Set : A:\PTO.SS.TXT

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L:12 M:201 W: Mandatory field.data missing, <130> FILE REFERENCE
 L:14 M:270 C: Current Application Number differs, Replaced Current Application No
 L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:54 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
 L:57 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:10 SEQ:1
 L:92 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
 L:95 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:7 SEQ:2
 L:138 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
 L:141 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:9 SEQ:3
 L:148 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:150 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:151 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
 L:151 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:4
 L:158 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:160 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:161 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
 L:161 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:5
 L:168 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:170 M:342 E: Invalid Stop Code On Error, STOP CODON:/*
 L:170 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:171 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
 L:171 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:14 SEQ:6
 L:178 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:180 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:184 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
 L:184 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:20 SEQ:7
 L:192 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:194 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:195 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
 L:195 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:8
 L:202 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:204 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:205 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
 M:332 Repeated in SeqNo=9
 L:208 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:9
 L:216 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:218 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:219 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
 L:222 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:18 SEQ:10
 L:230 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:232 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:233 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
 L:236 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:18 SEQ:11
 L:244 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:246 M:333 E: Wrong sequence grouping, Amino acids not in groups!

VERIFICATION SUMMARY

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Input Set : A:\PTO.SS.TXT

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L:247 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
L:247 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:15 SEQ:12
L:254 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:256 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:257 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:13
L:257 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:10 SEQ:13
L:264 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:266 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:267 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:267 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:9 SEQ:14
L:274 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:276 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:277 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15
M:332 Repeated in SeqNo=15
L:280 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:22 SEQ:15
L:288 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:290 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:291 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:291 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:10 SEQ:16
L:298 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:300 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:301 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
M:332 Repeated in SeqNo=17
L:304 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:17
L:312 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:318 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:318 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18
L:318 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:22 SEQ:18
L:345 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:347 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:348 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
L:348 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:20
L:355 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:357 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:358 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
L:358 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:21
L:365 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:367 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:368 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:368 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:22
L:375 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:377 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:378 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:378 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:23
L:385 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:387 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:388 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24
L:388 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:24
L:395 M:282 E: Numeric Field Identifier Missing, <211> is required.

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L:397 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:398 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:25
 L:398 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:11 SEQ:25
 L:405 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:407 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:408 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26
 L:408 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:16 SEQ:26
 L:415 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:417 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:418 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
 L:418 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:13 SEQ:27
 L:425 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:427 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:428 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:28
 M:332 Repeated in SeqNo=28
 L:431 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:21 SEQ:28
 L:439 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:441 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:442 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:29
 L:445 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:16 SEQ:29
 L:453 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:455 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:456 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:30
 L:456 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:14 SEQ:30
 L:463 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:465 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:469 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
 L:469 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:17 SEQ:31
 L:477 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:479 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:480 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
 L:480 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:14 SEQ:32
 L:506 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:508 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:509 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:34
 M:332 Repeated in SeqNo=34
 L:513 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:21 SEQ:34
 L:521 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:523 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:524 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
 L:524 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:35
 L:531 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:533 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:534 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
 L:534 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:10 SEQ:36
 L:541 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:543 M:342 E: Invalid Stop Code On Error, STOP CODON:/*
 L:543 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:544 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:37

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L:544 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:14 SEQ:37
 L:551 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:553 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:557 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:557 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
 L:561 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
 M:332 Repeated in SeqNo=38
 L:561 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:43 SEQ:38
 L:568 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:570 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:571 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
 L:571 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:39
 L:578 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:580 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:581 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
 L:581 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:9 SEQ:40
 L:588 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:591 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
 L:594 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 M:332 Repeated in SeqNo=41
 L:594 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:26 SEQ:41
 L:602 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:608 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:609 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
 L:609 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:30 SEQ:42
 L:616 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:622 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:623 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
 L:623 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:31 SEQ:43
 L:630 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:636 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:636 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
 L:636 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:44
 L:644 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:646 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:647 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
 L:647 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:45
 L:654 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:656 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:657 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
 M:332 Repeated in SeqNo=46
 L:660 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:18 SEQ:46
 L:668 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:670 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:671 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:47
 L:674 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:17 SEQ:47
 L:682 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:684 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:686 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:15 SEQ:48

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L:693 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:699 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:703 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:35 SEQ:49
L:711 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:717 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:717 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:50
L:725 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:731 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:731 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:23 SEQ:51
L:739 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:741 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:742 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:12 SEQ:52
L:751 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:761 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
L:911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 after pos.:0
L:1018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68 after pos.:0
L:1044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69 after pos.:0
L:1072 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:0
L:1101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71 after pos.:0